

1 TCAAATTTT CTCCAGTTCT AAATATCCGG AAACCTCTTG GGATGCCATT
 -----A-----
 51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT
 -----B-----|-----C-----|---D---
 101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC
 -----E-----|-----F-----|
 151 TCTGCTGACA TTGGTCCCCA AGTGAAGCA CCACCCCATG AGGAGCACCG
 -----G-----|-----H-----|-----
 201 TGGAGTAAGA AGACGTTCGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT
 --F--|-----G-----|-----I-----
 251 AGTATCTCCA TTGACGTAAG GGATGAACAA CAATCCAAC TCCATCGCA
 -----J-----|-----K-----|-----L-----
 301 AGACCATTC TCTATATAAG AAAGTTAATA TCATTTCGAG TGGCCACGCT
 -----M-----|-----L-----|---N---
 351 G [SEQ ID NO:1]

FIGURE 1

1 TCAAATTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT
51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT
101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC
151 TCTGCTGACA TTGGTCCCCA AGTGAAGCA CCACCCCATG AGGAGCACCG
201 TGGAGTAAGA AGACGTTCGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT
251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAACT ATCCATCGCA
301 AGACCATTGC TCTATATAAG AAGTTAATA TCATTTCGAG TGGCCACGCT
351 G [SEQ ID NO:2]

FIGURE 2

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1   TCAAATTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT
    ||||| ||| ||||| ||| ||||| |||||
TGAGACTTTT CAACAAAGGG TAATATCGGG AACCTCCCTC GGATTCCATT

51  GCCCATCTAT CTGT-AATTT ATTGACGAAA TAGACGAAAA GGAAGGTGGC
    ||||| ||| ||| ||| ||| ||| ||| ||| |||
GCCCAGCTAT CTGTCACTTC ATCAAAGGA CAGTAGAAAA GGAAGGTGGC

101 TCCTATAAAG CACATCATTTG CGATAACAGA AAGGCCATTG TTGAAGATAC
    ||||| ||| ||||| ||| ||||| ||| ||||| |||
ACCTACAAAT GCCATCATTTG CGATAAAGGA AAGGCTATCG TTCAAGATGC

151 CTCTGCTGAC ATTGGTCCCC AAGTGGAAGC ACCACCCCAT GAGGAGCACC
    ||||| ||| ||||| ||| ||||| ||| ||||| |||
CTCTGCCGAC AGTGGTCCCA AAGATGGACC CCCA-CCCAC GAGGAGCATC

201 GTGGAGTAAG AAGACGTTTCG AGCCACGTCG AAAAAGCAAG TGTGTTGATG
    ||||| ||| ||||| ||| ||||| ||| ||||| |||
GTGGAAAAAG AAGACGTTTC AACCACGTC TCAAAGCAAG TGGATTGATG

251 TAGTATCTCC ATTGACGTAA GGGATGACGC ACAATCCAAC TATCCATCGC
    ||||| ||| ||||| ||| ||||| ||| ||||| |||
TCATATCTCC ACTGACGTAA GGGATGACGC ACAATCCAC TATCCTTCGC

301 AAGACCATTG CTCTATATAA GAAAGTTAAT ATCATTTTGA GTGGCCACGC
    ||||| ||| ||||| ||| ||||| ||| ||||| |||
AAGACCCTTC CTCTATATAA GGAAGTTCAT TTCATTTTGA GAGGACACGC

351 TG [SEQ ID NO:2]
    ||
TG [SEQ ID NO:3]
  
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FIGURE 3



FIG. 4A

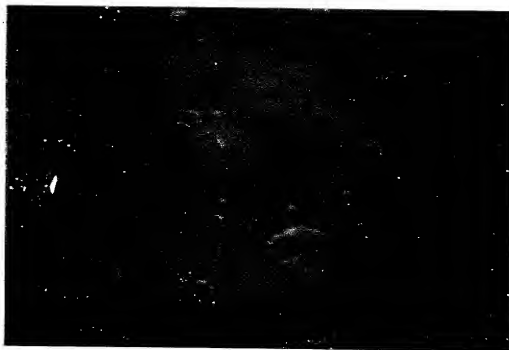


FIG. 4B